selectivity of inhibitory ligands, their susceptibility to resistance mutations, and the discovery of putative allosteric binding sites. Markov state models have recently emerged as a practical computational approach to the enumeration of protein conformational states, and can be constructed by aggregating the data from multiple, independent, short molecular dynamics trajectories in a statistical fashion. We aim to apply this technique to the entire human kinome, simulating each protein kinase catalytic domain using a range of high performance compute resources, including the distributed simulation framework, Folding@Home. In combination with recent developments in GPU-accelerated simulation algorithms, this approach allows us to obtain aggregate trajectory lengths on the order of milliseconds. An automated software pipeline provides the ability to quickly generate multiple starting configurations for each kinase, while a central database of publicly available kinase data has been set up and used for tasks such as the selection of catalytic domain sequences and the assignment of relative priorities to each kinase. In parallel with our computational approach, we are working towards expressing a diverse range of kinases in bacterial systems, and scaling up a fluorescence-based assay to plate format for direct measurement of kinase inhibitor binding affinities. Our poster will present preliminary results from these efforts.

3316-Pos Board B44
Docking Benchmark Set of Protein Models
Ivan Anishchanka[1,2], Petras J. Kundrotas[1], Alexander V. Tuzikov[2], Ilya A. Vakser[1,3].
[1]Center for Bioinformatics, The University of Kansas, Lawrence, KS, USA, [2]National Academy of Sciences of Belarus, Minsk, Belarus, [3]Department of Molecular Biosciences, The University of Kansas, Lawrence, KS, USA.
Protein docking is a computational procedure for predicting the 3D structure of protein complexes. Docking has been extensively benchmarked on experimentally determined protein structures. However, studies of protein-protein interactions increasingly involve modeled structures of the individual interactors. These structures are inherently less accurate than the X-ray structures. Thus, the utility of docking procedures, when applied to protein models, should be thoroughly tested in benchmarking studies. Such benchmark set of protein models was developed as part of the DOCKGROUND resource (http://dockground.bioinformatics.ku.edu). The set contains 63 complexes with each monomer represented by six models with a pre-defined Ca RMSD from the native structure (1, 2, … 6 Å). The models were generated by a combination of homology modeling and Nudged Elastic Band method. A new, extended set of protein models was recently built for 165 nonredundant hetero complexes from DOCKGROUND. For more realistic representation of the models, they were generated exclusively by I-TASSER protein modeling package. The benchmark sets were used in the assessment of protein docking methodologies.

3317-Pos Board B45
Structural Similarity in Modeling of Homodimers
Petras Kundrotas[1], Ilya Vakser[1], Joël Janin[2].
[1]University of Kansas, LAWRENCE, KS, USA, [2], Université Paris-Sud 11, Orsay, France.
Template-based methods, which utilize known protein structures, are commonly employed to model individual proteins from their sequences. Here we benchmark a template-based method, previously proposed for modeling hetero-dimeric complexes, on sets of homodimeric assemblies. The method is based on structural alignment of assembly subunits and identifies templates for the vast majority of the test targets. In many cases, the target-template pairs have sequence identity too low for reliable detection by sequence-based methods. An overall dimer geometry as well as interface residue contacts are correctly reproduced for almost half of the targets. We present analysis of the obtained models and their templates, which revealed incorrectly determined quaternary structure for a number of entries in the Protein Data Bank.

3318-Pos Board B46
Three-Dimensional Structure of the 54-Kda Subunit of the Chloroplast Signal Recognition Particle using Molecular Modeling
Rory Henderson, Mercede Furr, Srinivas Jayanthi, Alicia Brown, Robyn Goforth, Ralph Henry, T.K.S. Kumar.
University of Arkansas, Fayttevile, AR, USA.
The chloroplast signal recognition particle is a heterodimeric complex of the 54kDa cytosolic signal recognition particle homologue (cpSRP54), and a novel 43kDa subunit (cpSRP43). While a nearly complete three-dimensional structure of cpSRP43 has been obtained, no structure is yet available for cpSRP54. The three-dimensional structure for cpSRP54 could provide valuable information for the rationalization of the extensive information already available regarding its function, and in the understanding of the as yet undetermined mechanism of light harvesting chlorophyll binding protein's (LHCP) insertion into the thylakoid membrane. In this study, we developed an in silico, three-dimensional structural model of cpsRP54 using a combination of homology modeling, de novo structure prediction and molecular dynamics simulation. The resulting structure is consistent with the known properties of the protein and sheds new light on some of the mechanistic details of its functioning.

3319-Pos Board B47
A Molecular Dynamics Simulation Study of Outer Membrane Phospholipase a (OMPLA) Structure and Dynamics in an Asymmetric Lipopolysaccharide Membrane
Emilia L. Wu[1], Patrick J. Fleming[2], Jeffery B. Klauda[3], Karen G. Fleming[2], Wonpil Im[1].
[1]University of Kansas, Lawrence, KS, USA, [2]John Hopkins University, Baltimore, MD, USA, [3]The University of Maryland, College Park, MD, USA.
The outer membrane of Gram-negative bacteria is a unique and highly asymmetric lipid bilayer composed of phospholipids in the inner leaflet and mostly lipopolysaccharide (LPS) in the outer leaflet. Outer membrane phospholipase A (OmpLA) is an integral membrane enzyme in Escherichia coli. The structure of monomeric OmpLA consists of a 12-stranded antiparallel β-strands with a convex and a flat side, six loops at the extracellular side and five turns at the periplasmic side of the membrane. Utilizing the latest C36 CHARMM lipid and carbohydrate force field, we have constructed a model of OmpLA embedded in an asymmetric lipid bilayer with rough LPS molecules (without O-antigen) in one leaflet and phosphatidylethanolamine, phosphatidylglycerol, and cardiolipin in the other leaflet to model the realistic outer membrane environment. The simulation results will be discussed in terms of the key structural properties of the bacterial outer membrane including hydrophobic thickness, area per lipid, and acyl chain order parameter. We will also show the difference of OmpLA structure and dynamics compared to that in a DLPC bilayer. At the same time a comparison between simulations with different numbers of LPS molecules on the outer leaflet will elucidate the potential technical difficulties in building asymmetric bilayer.

3320-Pos Board B48
Modular Platform for Biomolecular Modeling and Simulations
Dominik Gront.
Faculty of Chemistry, University of Warsaw, Warsaw, Poland.
Computational software has been a cornerstone of many biological sciences such as biophysics, bioinformatics or biomolecular modelling in general. The last few decades witnessed numerous software packages that implemented newly emerging methods and algorithms. In parallel with the development of methods to solve particular scientific problems, the general picture how a suite of computational software should be constructed also evolved.
Here we present the design, implementation and functionality of BioShell[1,2] software - a versatile package for biomolecular modelling. Its functionality ranges from processing structural and sequence databases to sampling conformations both in Cartesian and alignment space. Highly modular structure facilitates easy extension of the package. Its modules may be conveniently bound by a high-level Python script into a single pipeline.
One of the newest BioShell applications is three-dimensional threading. A Monte Carlo search scheme samples the conformational space of alignments between a query sequence and a template structure. In another example, BioShell modules were used to build a simple computational model of RNA molecules.
1. D. Gront, and A. Kolinski, Bioinformatics, 2005, 22, 621-622.
2. D. Gront, and A. Kolinski, Bioinformatics, 2008, 24, 584-585.

3321-Pos Board B49
A Global Machine Learning Based Scoring Function for Protein Structure Prediction
Eshel Faraggi[1,2], **Andrzej Kloczkowski**[2,3].
[1]Department of Biochemistry and Molecular Biology, Indiana University School of Medicine, Indianapolis, IN, USA, [2]Battelle Center for Mathematical Medicine, Nationwide Children's Hospital, Columbus, OH, USA, [3]Department of Pediatrics, The Ohio State University, Columbus, OH, USA.
We present a knowledge-based function to score protein decoys based on their similarity to native structure. A set of features is constructed to describe the structure and sequence of the entire protein chain. Furthermore, a qualitative relationship is established between the calculated features and the underlying electromagnetic interaction that dominates this scale. The features we use are associated with residue-residue distances, residue-solvent distances, pairwise knowledge based potentials and a four-body potential. In addition we introduce a new target to be predicted, the fitness score, which measures the similarity of a model to the native structure. This new approach enables us to obtain information both from decoys and from native structures. It is also devoid of